

REMARKS

The Examiner has acknowledged Applicants' election of Group IV and species (c), (e), (f), and (h). Claims 8-9, 11-17, and 45-51 have been withdrawn as being drawn to a nonelected group. The Examiner, therefore, concludes that claims 1-7, 10, and 18-44 (Figure 4) are under consideration. For the sake of clarity, however, Applicants refer the Examiner to the Preliminary Amendment submitted at the time of filing in the United States, wherein amendments to the claims were presented, claims 11-17 and 35-38 were canceled, and new claim 51 was added. Accordingly, claims 1-7, 10, 18-34, and 39-44 (Figure 4) are under consideration.

Claims 1-4 and 7 have been amended to improve clarity and correct minor typographical errors. Claims 1 and 3 have been amended to clarify the numbering of the amino acid residues at positions I-IV of the first binding site. Specifically, claims 1 and 3 have been amended to replace recited residues "122, 54, 50 and 95" with residues "139, 71, 67, and 112". The discrepancy in numbering with regard to positions I-IV of the first binding site, which amounts to a consistent differential of 17 amino acids, stemmed from the difference in length observed between the full length protein, which comprises an N-terminal leader sequence, and the mature protein, from which the leader sequence has been processed or removed. SEQ ID NO: 4 which is presented in Figure 4 depicts the amino acid sequence of the full length protein. As a consequence, the numerical delineations of positions I-IV of the first binding site are, accordingly, shifted by 17 residues.

Claims 2 and 3 have been amended to clarify the numbering of the amino acid residues at positions I-IV of the second binding site. Specifically, claims 2 and 3 have been amended to replace recited residues "112, 149, 35 and 135" with residues "129, 166, 52 and 152". As set forth above with regard to positions I-IV of the first binding site, positions I-IV of the second binding site were originally presented with regard to the shorter, mature protein. As is evident from the specification and drawings, in particular Figures 4 and 22, positions I-IV of the second binding site correspond to residues 129, 166, 52 and 152 of the full length protein as shown in Figure 4. Support for the amendment to claims 1-3 is presented throughout the specification and in the Figures as indicated herein above.

Claim 4 has been amended to correct a clerical error. Claim 7 has been amended to

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rectify a grammatical error. No new matter is introduced by these amendments.

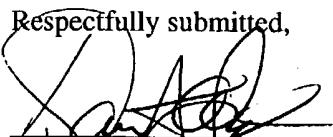
By this Office Action, the Examiner has required restriction within the formerly presented Invention of Group IV (claims 1-7, 10, 18-44; Figure 4). The Examiner contends that claims 1-7, 10, and 18-44 are drawn to numerous species. Specifically, the Examiner maintains that the claims of Invention IV pertain to eleven (11) species corresponding to each of SEQ ID Nos: 1-11.

Responsive to the Requirement for restriction, Applicants elect to prosecute the single species of SEQ ID NO: 4, which is set forth in Figure 4.

No additional fees are believed to be necessitated by the foregoing Response. However, should this be erroneous, authorization is hereby given to charge Deposit Account No. 11-1153 for any underpayment, or credit any overages.

In view of the above, withdrawal of the Requirement for the Restriction is requested, and an early action on the merits of the Claims is courteously solicited.

Respectfully submitted,

  
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Date: August 29, 2003

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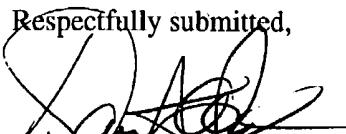
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*a<sup>4</sup>* 50. (Amended) A transgenic animal that has been transformed by a nucleic acid molecule according to [either of] claim[s] 45 [or 46 or vector according to either of claims 47 or 48].

Please add the following new Claim 51:

*a<sup>5</sup>* 51. A protein selected from the group consisting of the Ra-Res amino acid sequence given in Figure 5, the Av-HBP amino acid sequence given in Figure 6, the Ih/Bm-HBP amino acid sequence given in Figure 7, the Ih/Bm-HBP2 amino acid sequence given in Figure 8, the Ih/Bm-HBP3 amino acid sequence given in Figure 9, the Ih/Bm-HBP4 amino acid sequence given in Figure 10, the Ih/Bm-HBP5 amino acid sequence given in Figure 11, functional equivalent derivatives or fragments thereof.

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The above amendments are submitted herewith to reduce multiple dependencies and to conform the claims more closely to U.S. practice.

The amendments made herein are with respect to Claims 1-50, which claims were amended during the pendency of the International Application. A copy of Claims 1-50, which are included in the International Preliminary Examination Report, are enclosed herewith and attached hereto.